

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/650,467A  
Source: 1Fu16  
Date Processed by STIC: 9/5/06

***ENTERED***



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/650,467A

DATE: 09/05/2006  
TIME: 12:42:22

Input Set : E:\6223nd1us.txt  
Output Set: N:\CRF4\09052006\J650467A.raw

3 <110> APPLICANT: Lowery, David E.  
4 Geary, Timothy G.  
5 Kubiak, Teresa M.  
6 Larsen, Martha J.  
8 <120> TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS  
10 <130> FILE REFERENCE: 30773/6223ND1US  
12 <140> CURRENT APPLICATION NUMBER: US 10/650,467A  
13 <141> CURRENT FILING DATE: 2003-08-28  
15 <160> NUMBER OF SEQ ID NOS: 243  
17 <170> SOFTWARE: PatentIn Ver. 2.0  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 1157  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Homo sapiens  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (1)..(1155)  
28 <220> FEATURE:  
29 <223> OTHER INFORMATION: Clone identifier: CEGPCR1a  
31 <400> SEQUENCE: 1  
32 atg aac ttt tcg gcc acc gat tcg ata ttg gca tca acg ata aca acg 48  
33 Met Asn Phe Ser Ala Thr Asp Ser Ile Leu Ala Ser Thr Ile Thr Thr  
34 1 5 10 15  
36 gtg att ggt gga gct gga gtt ttg gca gaa gca ggc gaa gct gaa cta 96  
37 Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu  
38 20 25 30  
40 tct ggt gat gat gat ttt tat gag ctg act cct gta gaa ttg ata ata 144  
41 Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile  
42 35 40 45  
44 tgg tgc atg ctg tat gca att ata gcc ttc atg gca gtt gtt gga aat 192  
45 Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn  
46 50 55 60  
48 ctt ctg gtt ctc tac ata aca ctg ttc aga tta aga gtc cgt tcc atc 240  
49 Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile  
50 65 70 75 80  
52 aca acc tac ttc att ctg aac ctc gga ttt gct gac ctc ttc act ggt 288  
53 Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly  
54 85 90 95  
56 att ttt gcg att ccc ttc aag ttt cag gct gct ctt ttt caa gaa tgg 336  
57 Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp  
58 100 105 110  
60 ttc ctg ccg cga tca ctc tgc cgg ata gtt cca tac gtg gaa aca gtt 384  
61 Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val

See  
P. 6

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/650,467A

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Input Set : E:\6223ndlus.txt

Output Set: N:\CRF4\09052006\J650467A.raw

62	115	120	125	
64	gct ctg aca gtt tca gtc ttc aca ctt gtg acg tca gca gtt cat gaa			432
65	Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu			
66	130	135	140	
68	ttc cgt aca atg ttc ttc tcg aaa tgc tca caa atg agc cca aga tct			480
69	Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser			
70	145	150	155	160
72	gca aaa cga tgt gta ctt ttg ata tgg ata atg gcg gtt ctt gtg tct			528
73	Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser			
74	165	170	175	
76	cta cca cat gga ttg ttc cat aat aca tac gaa ttt cca gat gac aat			576
77	Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn			
78	180	185	190	
80	aat act tca att gta cag tgt ctc cca gta tat cct gat gct ggt tgg			624
81	Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp			
82	195	200	205	
84	tgg aaa aca tac aat gtc tac ctt gtc ata atc caa tat ttt gtt cca			672
85	Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro			
86	210	215	220	
88	atg att att ctt gac act gcg tac aca atg att gct gtt aaa ata tgg			/20
89	Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp			
90	225	230	235	240
92	tca ttg agt cag tca aga gtt gaa ctt gat gaa aca aaa atg gca acc			768
93	Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr			
94	245	250	255	
96	cag aag ctt atg cgt act ctc atc att gtc gtt gcc tgt ttc tca ttg			816
97	Gln Lys Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu			
98	260	265	270	
100	tgt tgg ttt cca ttg gag acg tat cta ctt ttg aat gaa ttg aaa ccg			864
101	Cys Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro			
102	275	280	285	
104	gaa att aat gga tgg aaa tac atc aat ttg gtg ttc ttc ttt tca cat			912
105	Glu Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His			
106	290	295	300	
108	tgg ctg gcg atg agc aat tct tgt ctt aat cca att att tat gga ctt			960
109	Trp Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu			
110	305	310	315	320
112	tac aat aca aaa tac aac gag gaa tat cgt cgt ttg ttt cgc caa att			1008
113	Tyr Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile			
114	325	330	335	
116	gga tgc att tgg caa cgg cag aaa agt ttg gac gat tcg atg aaa ccg			1056
117	Gly Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro			
118	340	345	350	
120	gag cgt cgt tgg aat tct tca aat gat tgt caa gat caa cag gaa att			1104
121	Glu Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Glu Ile			
122	355	360	365	
126	gat caa att gtt gat att cca cca gtt att tct aca aat aat ctt tct			1152
127	Asp Gln Ile Val Asp Ile Pro Pro Val Ile Ser Thr Asn Asn Leu Ser			
128	370	375	380	

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Input Set : E:\6223ndlus.txt  
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130 ccc tg 1157  
 131 Pro  
 132 385  
 135 <210> SEQ ID NO: 2  
 136 <211> LENGTH: 385  
 137 <212> TYPE: PRT  
 138 <213> ORGANISM: Homo sapiens  
 140 <400> SEQUENCE: 2  
 141 Met Asn Phe Ser Ala Thr Asp Ser Ile Leu Ala Ser Thr Ile Thr Thr  
 142 1 5 10 15  
 144 Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu  
 145 20 25 30  
 147 Ser Gly Asp Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile  
 148 35 40 45  
 150 Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn  
 151 50 55 60  
 153 Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile  
 154 65 70 75 80  
 156 Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly  
 157 85 90 95  
 159 Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp  
 160 100 105 110  
 162 Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val  
 163 115 120 125  
 165 Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu  
 166 130 135 140  
 168 Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser  
 169 145 150 155 160  
 171 Ala Lys Arg Cys Val Leu Leu Ile Trp Ile Met Ala Val Leu Val Ser  
 172 165 170 175  
 174 Leu Pro His Gly Leu Phe His Asn Thr Tyr Glu Phe Pro Asp Asp Asn  
 175 180 185 190  
 177 Asn Thr Ser Ile Val Gln Cys Leu Pro Val Tyr Pro Asp Ala Gly Trp  
 178 195 200 205  
 180 Trp Lys Thr Tyr Asn Val Tyr Leu Val Ile Ile Gln Tyr Phe Val Pro  
 181 210 215 220  
 183 Met Ile Ile Leu Asp Thr Ala Tyr Thr Met Ile Ala Val Lys Ile Trp  
 184 225 230 235 240  
 186 Ser Leu Ser Gln Ser Arg Val Glu Leu Asp Glu Thr Lys Met Ala Thr  
 187 245 250 255  
 189 Gln Lys Leu Met Arg Thr Leu Ile Ile Val Val Ala Cys Phe Ser Leu  
 190 260 265 270  
 192 Cys Trp Phe Pro Leu Glu Thr Tyr Leu Leu Leu Asn Glu Leu Lys Pro  
 193 275 280 285  
 195 Glu Ile Asn Gly Trp Lys Tyr Ile Asn Leu Val Phe Phe Phe Ser His  
 196 290 295 300  
 198 Trp Leu Ala Met Ser Asn Ser Cys Leu Asn Pro Ile Ile Tyr Gly Leu  
 199 305 310 315 320  
 201 Tyr Asn Thr Lys Tyr Asn Glu Glu Tyr Arg Arg Leu Phe Arg Gln Ile

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/650,467A

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Input Set : E:\6223nd1us.txt

Output Set: N:\CRF4\09052006\J650467A.raw

202 325 330 335  
 204 Gly Cys Ile Trp Gln Arg Gln Lys Ser Leu Asp Asp Ser Met Lys Pro  
 205 340 345 350  
 207 Glu Arg Arg Trp Asn Ser Ser Asn Asp Cys Gln Asp Gln Gln Glu Ile  
 208 355 360 365  
 210 Asp Gln Ile Val Asp Ile Pro Pro Val Ile Ser Thr Asn Asn Leu Ser  
 211 370 375 380

213 Pro

214 385

217 &lt;210&gt; SEQ ID NO: 3

218 &lt;211&gt; LENGTH: 1202

219 &lt;212&gt; TYPE: DNA

220 &lt;213&gt; ORGANISM: Homo sapiens

222 &lt;220&gt; FEATURE:

223 &lt;221&gt; NAME/KEY: CDS

224 &lt;222&gt; LOCATION: (1)..(1200)

226 &lt;220&gt; FEATURE:

227 &lt;223&gt; OTHER INFORMATION: Clone identifier: CEGPCR1f

229 &lt;400&gt; SEQUENCE: 3

230 aty aac ttt tcg gcc acc gat tcg ata ttg gca tca acg ata aca acg	48
231 Met Asn Phe Ser Ala Thr Asp Ser Ile Leu Ala Ser Thr Ile Thr Thr	
232 1 5 10 15	
234 gtg att ggt gga gct gga gtt ttg gca gaa gca ggc gaa gct gaa cta	96
235 Val Ile Gly Gly Ala Gly Val Leu Ala Glu Ala Gly Glu Ala Glu Leu	
236 20 25 30	
238 tct ggt gat gat gat ttt tat gag ctg act cct gta gaa ttg ata ata	144
239 Ser Gly Asp Asp Phe Tyr Glu Leu Thr Pro Val Glu Leu Ile Ile	
240 35 40 45	
242 tgg tgc atg ctg tat gca att ata gcc ttc atg gca gtt gtt gga aat	192
243 Trp Cys Met Leu Tyr Ala Ile Ile Ala Phe Met Ala Val Val Gly Asn	
244 50 55 60	
246 ctt ctg gtt ctc tac ata aca ctg ttc aga tta aga gtc cgt tcc atc	240
247 Leu Leu Val Leu Tyr Ile Thr Leu Phe Arg Leu Arg Val Arg Ser Ile	
248 65 70 75 80	
251 aca acc tac ttc att ctg aac ctc gga ttt gct gac ctc ttc act ggt	288
252 Thr Thr Tyr Phe Ile Leu Asn Leu Gly Phe Ala Asp Leu Phe Thr Gly	
253 85 90 95	
255 att ttt gcg att ccc ttc aag ttt cag gct gct ctt ttt caa gaa tgg	336
256 Ile Phe Ala Ile Pro Phe Lys Phe Gln Ala Ala Leu Phe Gln Glu Trp	
257 100 105 110	
259 ttc ctg ccg cga tca ctc tgc cgg ata gtt cca tac gtg gaa aca gtt	384
260 Phe Leu Pro Arg Ser Leu Cys Arg Ile Val Pro Tyr Val Glu Thr Val	
261 115 120 125	
263 gct ctg aca gtt tca gtc ttc aca ctt gtg acg tca gca gtt cat gaa	432
264 Ala Leu Thr Val Ser Val Phe Thr Leu Val Thr Ser Ala Val His Glu	
265 130 135 140	
267 ttc cgt aca atg ttc ttc tcg aaa tgc tca caa atg agc cca aga tct	480
268 Phe Arg Thr Met Phe Phe Ser Lys Cys Ser Gln Met Ser Pro Arg Ser	
269 145 150 155 160	

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271	gca	aaa	cga	tgt	gta	ctt	ttg	ata	tgg	ata	atg	gcg	gtt	ctt	gtg	tct	528	
272	Ala	Lys	Arg	Cys	Val	Leu	Leu	Ile	Trp	Ile	Met	Ala	Val	Leu	Val	Ser		
273								165			170					175		
275	cta	cca	cat	gga	ttg	ttc	cat	aat	aca	tac	gaa	ttt	cca	gat	gac	aat	576	
276	Leu	Pro	His	Gly	Leu	Phe	His	Asn	Thr	Tyr	Glu	Phe	Pro	Asp	Asp	Asn		
277								180			185					190		
279	aat	act	tca	att	gta	cag	tgt	ctc	cca	gta	tat	cct	gat	gct	ggt	tgg	624	
280	Asn	Thr	Ser	Ile	Val	Gln	Cys	Leu	Pro	Val	Tyr	Pro	Asp	Ala	Gly	Trp		
281								195			200					205		
283	tgg	aaa	aca	tac	aat	gtc	tac	ctt	gtc	ata	atc	caa	tat	ttt	gtt	cca	672	
284	Trp	Lys	Thr	Tyr	Asn	Val	Tyr	Leu	Val	Ile	Ile	Gln	Tyr	Phe	Val	Pro		
285								210			215					220		
287	atg	att	att	ctt	gac	act	gcg	tac	aca	atg	att	gct	gtt	aaa	ata	tgg	720	
288	Met	Ile	Ile	Leu	Asp	Thr	Ala	Tyr	Thr	Met	Ile	Ala	Val	Lys	Ile	Trp		
289	225						230				235					240		
291	tca	ttg	agt	cag	tca	aga	gtt	gaa	ctt	gat	gaa	aca	aaa	atg	gca	acc	768	
292	Ser	Leu	Ser	Gln	Ser	Arg	Val	Glu	Leu	Asp	Glu	Thr	Lys	Met	Ala	Thr		
293								245			250					255		
295	cag	aag	ata	tca	gtg	gtt	tca	atg	gtt	tca	cca	aac	act	caa	tta	tcg	816	
296	Gln	Lys	Ile	Ser	Val	Val	Ser	Met	Val	Ser	Pro	Asn	Thr	Gln	Leu	Ser		
297								260			265					270		
299	cag	ctt	atg	cgt	act	ctc	atc	att	gtc	gtt	gcc	tgt	ttc	tca	ttg	tgt	864	
300	Gln	Leu	Met	Arg	Thr	Leu	Ile	Ile	Val	Val	Ala	Cys	Phe	Ser	Leu	Cys		
301							275			280					285			
303	tgg	ttt	cca	ttg	gag	acg	tat	cta	ctt	ttg	aat	gaa	ttg	aaa	ccg	gaa	912	
304	Trp	Phe	Pro	Leu	Glu	Thr	Tyr	Leu	Leu	Leu	Asn	Glu	Leu	Lys	Pro	Glu		
305							290			295					300			
307	att	aat	gga	tgg	aaa	tac	atc	aat	ttg	gtg	ttc	ttc	ttt	tca	cat	tgg	960	
308	Ile	Asn	Gly	Trp	Lys	Tyr	Ile	Asn	Leu	Val	Phe	Phe	Phe	Ser	His	Trp		
309	305							310			315					320		
313	ctg	gcg	atg	agc	aat	tct	tgt	ctt	aat	cca	att	att	tat	gga	ctt	tac	1008	
314	Leu	Ala	Met	Ser	Asn	Ser	Cys	Leu	Asn	Pro	Ile	Ile	Tyr	Gly	Leu	Tyr		
315								325			330					335		
317	aat	aca	aaa	tac	aac	gag	gaa	tat	cgt	cgt	ttg	ttt	ccg	caa	att	gga	1056	
318	Asn	Thr	Lys	Tyr	Asn	Glu	Glu	Tyr	Arg	Arg	Leu	Phe	Arg	Gln	Ile	Gly		
319							340			345					350			
321	tgc	att	tgg	caa	ccg	cag	aaa	agt	ttg	gac	gat	tcg	atg	aaa	ccg	gag	1104	
322	Cys	Ile	Trp	Gln	Arg	Gln	Lys	Ser	Leu	Asp	Asp	Ser	Met	Lys	Pro	Glu		
323							355			360					365			
325	cgt	cgt	tgg	aat	tct	tca	aat	gat	tgt	caa	gat	caa	cag	gaa	att	gat	1152	
326	Arg	Arg	Trp	Asn	Ser	Ser	Asn	Asp	Cys	Gln	Asp	Gln	Gln	Glu	Ile	Asp		
327							370			375					380			
329	caa	att	gtt	gat	att	cca	cca	gtt	att	tct	aca	aat	aat	ctt	tct	ccc	1200	
330	Gln	Ile	Val	Asp	Ile	Pro	Pro	Val	Ile	Ser	Thr	Asn	Asn	Leu	Ser	Pro		
331	385						390				395					400		
333	tg															1202		
336	<210>	SEQ	ID	NO:	4													
337	<211>	LENGTH:	400															
338	<212>	TYPE:	PRT															

**RAW SEQUENCE LISTING ERROR SUMMARY**      **DATE:** 09/05/2006  
**PATENT APPLICATION:** US/10/650,467A      **TIME:** 12:42:23

Input Set : E:\6223ndlus.txt  
Output Set: N:\CRF4\09052006\J650467A.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:90; Xaa Pos. 3  
Seq#:95; Xaa Pos. 1  
Seq#:103; Xaa Pos. 1  
Seq#:118; Xaa Pos. 1  
Seq#:119; Xaa Pos. 1  
Seq#:160; Xaa Pos. 1  
Seq#:162; Xaa Pos. 1  
Seq#:164; Xaa Pos. 1

## VERIFICATION SUMMARY

DATE: 09/05/2006

PATENT APPLICATION: US/10/650,467A

TIME: 12:42:23

Input Set : E:\6223nd1us.txt

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L:1936 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:  
L:1944 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:  
L:5313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:0  
L:5398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:0  
L:5525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:0  
L:7025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118 after pos.:0  
L:7049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:119 after pos.:0  
L:7120 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (124) SEQUENCE:  
L:7204 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (130) SEQUENCE:  
L:7228 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (132) SEQUENCE:  
L:7253 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (134) SEQUENCE:  
L:7308 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (138) SEQUENCE:  
L:7333 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (140) SEQUENCE:  
L:7357 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (142) SEQUENCE:  
L:7381 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (144) SEQUENCE:  
L:7391 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (145) SEQUENCE:  
L:7400 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (146) SEQUENCE:  
L:7409 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (147) SEQUENCE:  
L:7418 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (148) SEQUENCE:  
L:7427 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (149) SEQUENCE:  
L:7642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:160 after pos.:0  
L:7685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:162 after pos.:0  
L:7728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:164 after pos.:0  
L:7790 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (168) SEQUENCE:  
L:7803 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (169) SEQUENCE:  
L:7815 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (170) SEQUENCE:

**STATISTICS SUMMARY**

PATENT APPLICATION: US/10/650,467A

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Input Set : E:\6223ndlus.txt

Output Set: N:\CRF4\09052006\J650467A.raw

Application Serial Number: US/10/650,467A

Alpha or Numeric or Xml: Numeric

Application Class:

Application File Date: 08-28-2003

Art Unit: IFW16

Software Application: PatentIN2.0

Total Number of Sequences: 243

Total Nucleotides: 40338

Total Amino Acids: 14106

Number of Errors: 0

Number of Warnings: 26

Number of Corrections: 0

**MESSAGE SUMMARY**

300 W: 18 ((50) Intentionally skipped Sequence)

341 W: 8 ((46) "n" or "Xaa" used)